

RAW SEQUENCE LISTING

DATE: 04/25/2001

PATENT APPLICATION: US/09/813,459

TIME: 13:48:52

Input Set : N:\CrF3\RULE60\09813459.txt

Output Set: N:\CRF3\04252001\I813459.raw

ENTERED

SEQUENCE LISTING

4 (1) GENERAL INFORMATION:
6 (i) APPLICANT: Lee, Se-Jin
7 Cunningham, Noreen
9 (ii) TITLE OF INVENTION: GROWTH DIFFERENTIATION FACTOR-10
11 (iii) NUMBER OF SEQUENCES: 26
13 (iv) CORRESPONDENCE ADDRESS:
14 (A) ADDRESSEE: Spensley Horn Jubas & Lubitz
15 (B) STREET: 1880 Century Park East, Suite 500
16 (C) CITY: Los Angeles
17 (D) STATE: California
18 (E) COUNTRY: USA
19 (F) ZIP: 90067
21 (v) COMPUTER READABLE FORM:
22 (A) MEDIUM TYPE: Floppy disk
23 (B) COMPUTER: IBM PC compatible
24 (C) OPERATING SYSTEM: PC-DOS/MS-DOS
25 (D) SOFTWARE: PatentIn Release #1.0, Version #1.25
27 (vi) CURRENT APPLICATION DATA:
C--> 28 (A) APPLICATION NUMBER: US/09/813,459
C--> 29 (B) FILING DATE: 20-Mar-2001
30 (C) CLASSIFICATION:
32 (vii) PRIOR APPLICATION DATA:
33 (A) APPLICATION NUMBER: 08/624,635
34 (B) FILING DATE:
36 (viii) ATTORNEY/AGENT INFORMATION:
37 (A) NAME: Wetherell, Jr., Ph.D., John R.,
38 (B) REGISTRATION NUMBER: 31,678
39 (C) REFERENCE/DOCKET NUMBER: PD-3054
41 (ix) TELECOMMUNICATION INFORMATION:
42 (A) TELEPHONE: (619) 455-5100
43 (B) TELEFAX: (619) 455-5110
46 (2) INFORMATION FOR SEQ ID NO: 1:
48 (i) SEQUENCE CHARACTERISTICS:
49 (A) LENGTH: 36 base pairs
50 (B) TYPE: nucleic acid
51 (C) STRANDEDNESS: single
52 (D) TOPOLOGY: linear
54 (ii) MOLECULE TYPE: DNA (genomic)
57 (vii) IMMEDIATE SOURCE:
58 (B) CLONE: NSC1
60 (ix) FEATURE:
61 (A) NAME/KEY: CDS
62 (B) LOCATION: 1..36
65 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:
67 CCGGAATTCA ARGTNGAYTT YGCNGAYATH GGNTGG
69 (2) INFORMATION FOR SEQ ID NO: 2:

36

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71      (i) SEQUENCE CHARACTERISTICS:
72          (A) LENGTH: 33 base pairs
73          (B) TYPE: nucleic acid
74          (C) STRANDEDNESS: single
75          (D) TOPOLOGY: linear
77      (ii) MOLECULE TYPE: DNA (genomic)
80      (vii) IMMEDIATE SOURCE:
81          (B) CLONE: NSC2
83      (ix) FEATURE:
84          (A) NAME/KEY: CDS
85          (B) LOCATION: 1..33
88      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:
90 CCGGAATTCTC CANGCRCARC TYTCNACNGT CAT
92 (2) INFORMATION FOR SEQ ID NO: 3:
94      (i) SEQUENCE CHARACTERISTICS:
95          (A) LENGTH: 33 base pairs
96          (B) TYPE: nucleic acid
97          (C) STRANDEDNESS: single
98          (D) TOPOLOGY: linear
100     (ii) MOLECULE TYPE: DNA (genomic)
103     (vii) IMMEDIATE SOURCE:
104         (B) CLONE: NSC3
106     (ix) FEATURE:
107         (A) NAME/KEY: CDS
108         (B) LOCATION: 1..33
111     (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:
113 CCGGAATTCTC CANGCRCANG AYTACNACNGT CAT
115 (2) INFORMATION FOR SEQ ID NO: 4:
117     (i) SEQUENCE CHARACTERISTICS:
118         (A) LENGTH: 2322 base pairs
119         (B) TYPE: nucleic acid
120         (C) STRANDEDNESS: single
121         (D) TOPOLOGY: linear
123     (ii) MOLECULE TYPE: DNA (genomic)
126     (vii) IMMEDIATE SOURCE:
127         (B) CLONE: Murine GDF-10
129     (ix) FEATURE:
130         (A) NAME/KEY: CDS
131         (B) LOCATION: 126..1553
134     (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4:
136 TGGGGTCATC CGGGCTGTCC GAGTCCCACA GGGACAACTC CAGCCGCGGA CGAGGTGCAC
138 AGCCAACACT GAGCCCTCCT TGTCTGTTCT CCTGGGCTCA GACCCTTCAC CACCGTTACT
140 CAGCC ATG GCT CCA GGT CCT GCT CGG ATC AGC TTG GGG TCC CAG CTG
141     Met Ala Pro Gly Pro Ala Arg Ile Ser Leu Gly Ser Gln Leu
142     1          5          10
144 CTG CCC ATG GTG CCG CTG CTC CTG CTG CTG CGG GGC GCA GGC TGC GGC
145 Leu Pro Met Val Pro Leu Leu Leu Leu Leu Arg Gly Ala Gly Cys Gly
146 15          20          25          30
148 CAC AGG GGC CCC TCA TGG TCC TCA TTG CCC TCG GCA GCT GCC GGT CTG

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149	His	Arg	Gly	Pro	Ser	Trp	Ser	Ser	Leu	Pro	Ser	Ala	Ala	Ala	Gly	Leu	
150					35				40						45		
152	CAG	GGG	GAC	AGG	GAC	TCC	CAG	CAG	TCA	CCC	GGG	GAC	GCA	GCA	GCC	GCT	311
153	Gln	Gly	Asp	Arg	Asp	Ser	Gln	Gln	Ser	Pro	Gly	Asp	Ala	Ala	Ala	Ala	
154				50					55					60			
156	CTG	GGC	CCA	GGC	GCC	CAG	GAC	ATG	GTC	GCT	ATC	CAC	ATG	CTC	AGG	CTC	359
157	Leu	Gly	Pro	Gly	Ala	Gln	Asp	Met	Val	Ala	Ile	His	Met	Leu	Arg	Leu	
158				65				70					75				
160	TAT	GAG	AAG	TAC	AAC	CGA	AGA	GGT	GCT	CCA	CCG	GGA	GGA	GGC	AAC	ACC	407
161	Tyr	Glu	Lys	Tyr	Asn	Arg	Arg	Gly	Ala	Pro	Pro	Gly	Gly	Gly	Asn	Thr	
162			80				85					90					
164	GTC	CGA	AGC	TTC	CGT	GCC	CGG	CTG	GAA	ATG	ATC	GAC	CAA	AAG	CCT	GTG	455
165	Val	Arg	Ser	Phe	Arg	Ala	Arg	Leu	Glu	Met	Ile	Asp	Gln	Lys	Pro	Val	
166	95					100				105					110		
168	TAT	TTC	TTC	AAC	TTG	ACT	TCC	ATG	CAA	GAC	TCA	GAA	ATG	ATC	CTC	ACA	503
169	Tyr	Phe	Phe	Asn	Leu	Thr	Ser	Met	Gln	Asp	Ser	Glu	Met	Ile	Leu	Thr	
170				115					120					125			
172	GCC	GCC	TTC	CAC	TTC	TAC	TCA	GAA	CCT	CCA	CGG	TGG	CCC	CGG	GCT	GGT	551
173	Ala	Ala	Phe	His	Phe	Tyr	Ser	Glu	Pro	Pro	Arg	Trp	Pro	Arg	Ala	Gly	
174				130					135					140			
176	GAG	GTA	TTC	TGC	AAG	CCC	CGA	GCT	AAG	AAC	GCA	TCC	TGC	CGC	CTC	CTG	599
177	Glu	Val	Phe	Cys	Lys	Pro	Arg	Ala	Lys	Asn	Ala	Ser	Cys	Arg	Leu	Leu	
178			145					150					155				
180	ACC	CCA	GGG	CTG	CCT	GCA	CGC	TTG	CAC	CTA	ATC	TTC	CGC	AGT	CTT	TCC	647
181	Thr	Pro	Gly	Leu	Pro	Ala	Arg	Leu	His	Leu	Ile	Phe	Arg	Ser	Leu	Ser	
182		160				165					170						
184	CAG	AAC	ACC	GCC	ACT	CAG	GGG	CTG	CTC	CGC	GGG	GCC	ATG	GCC	CTG	ACG	695
185	Gln	Asn	Thr	Ala	Thr	Gln	Gly	Leu	Leu	Arg	Gly	Ala	Met	Ala	Leu	Thr	
186	175					180				185				190			
188	CCT	CCA	CCA	CGT	GGC	CTG	TGG	CAG	GCC	AAG	GAC	ATC	TCC	TCA	ATC	ATC	743
189	Pro	Pro	Pro	Arg	Gly	Leu	Trp	Gln	Ala	Lys	Asp	Ile	Ser	Ser	Ile	Ile	
190				195					200					205			
192	AAG	GCT	GCC	CGA	AGG	GAT	GGA	GAG	CTG	CTT	CTC	TCT	GCT	CAG	CTG	GAT	791
193	Lys	Ala	Ala	Arg	Arg	Asp	Gly	Glu	Leu	Leu	Leu	Ser	Ala	Gln	Leu	Asp	
194				210				215					220				
196	ACT	GGG	GAG	AAG	GAC	CCC	GGA	GTG	CCA	CGG	CCC	AGT	TCC	CAC	ATG	CCC	839
197	Thr	Gly	Glu	Lys	Asp	Pro	Gly	Val	Pro	Arg	Pro	Ser	Ser	His	Met	Pro	
198			225				230						235				
200	TAT	ATC	CTT	GTC	TAC	GCC	AAT	GAC	CTG	GCC	ATC	TCC	GAA	CCC	AAC	AGT	887
201	Tyr	Ile	Leu	Val	Tyr	Ala	Asn	Asp	Leu	Ala	Ile	Ser	Glu	Pro	Asn	Ser	
202		240				245					250						
204	GTA	GCA	GTG	TCG	CTA	CAG	AGA	TAC	GAC	CCA	TTT	CCA	GCT	GGA	GAC	TTT	935
205	Val	Ala	Val	Ser	Leu	Gln	Arg	Tyr	Asp	Pro	Phe	Pro	Ala	Gly	Asp	Phe	
206	255					260					265				270		
208	GAG	CCT	GGA	GCA	GCC	CCC	AAC	AGC	TCA	GCT	GAT	CCC	CGC	GTG	CGC	AGG	983
209	Glu	Pro	Gly	Ala	Ala	Pro	Asn	Ser	Ser	Ala	Asp	Pro	Arg	Val	Arg	Arg	
210				275					280					285			
212	GCG	GCT	CAG	GTG	TCA	AAA	CCC	CTG	CAA	GAC	AAT	GAA	CTG	CCG	GGG	CTG	1031
213	Ala	Ala	Gln	Val	Ser	Lys	Pro	Leu	Gln	Asp	Asn	Glu	Leu	Pro	Gly	Leu	

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290      (A) LENGTH: 476 amino acids
291      (B) TYPE: amino acid
292      (D) TOPOLOGY: linear
294      (ii) MOLECULE TYPE: protein
296      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5:
298 Met Ala Pro Gly Pro Ala Arg Ile Ser Leu Gly Ser Gln Leu Leu Pro
299   1      5      10      15
301 Met Val Pro Leu Leu Leu Leu Arg Gly Ala Gly Cys Gly His Arg
302      20      25      30
304 Gly Pro Ser Trp Ser Ser Leu Pro Ser Ala Ala Ala Gly Leu Gln Gly
305      35      40      45
307 Asp Arg Asp Ser Gln Gln Ser Pro Gly Asp Ala Ala Ala Ala Leu Gly
308      50      55      60
310 Pro Gly Ala Gln Asp Met Val Ala Ile His Met Leu Arg Leu Tyr Glu
311   65      70      75      80
313 Lys Tyr Asn Arg Arg Gly Ala Pro Pro Gly Gly Gly Asn Thr Val Arg
314      85      90      95
316 Ser Phe Arg Ala Arg Leu Glu Met Ile Asp Gln Lys Pro Val Tyr Phe
317      100     105     110
319 Phe Asn Leu Thr Ser Met Gln Asp Ser Glu Met Ile Leu Thr Ala Ala
320      115     120     125
322 Phe His Phe Tyr Ser Glu Pro Pro Arg Trp Pro Arg Ala Gly Glu Val
323      130     135     140
325 Phe Cys Lys Pro Arg Ala Lys Asn Ala Ser Cys Arg Leu Leu Thr Pro
326 145      150     155     160
328 Gly Leu Pro Ala Arg Leu His Leu Ile Phe Arg Ser Leu Ser Gln Asn
329      165     170     175
331 Thr Ala Thr Gln Gly Leu Leu Arg Gly Ala Met Ala Leu Thr Pro Pro
332      180     185     190
334 Pro Arg Gly Leu Trp Gln Ala Lys Asp Ile Ser Ser Ile Ile Lys Ala
335      195     200     205
337 Ala Arg Arg Asp Gly Glu Leu Leu Leu Ser Ala Gln Leu Asp Thr Gly
338      210     215     220
340 Glu Lys Asp Pro Gly Val Pro Arg Pro Ser Ser His Met Pro Tyr Ile
341 225      230     235     240
343 Leu Val Tyr Ala Asn Asp Leu Ala Ile Ser Glu Pro Asn Ser Val Ala
344      245     250     255
346 Val Ser Leu Gln Arg Tyr Asp Pro Phe Pro Ala Gly Asp Phe Glu Pro
347      260     265     270
349 Gly Ala Ala Pro Asn Ser Ser Ala Asp Pro Arg Val Arg Arg Ala Ala
350      275     280     285
352 Gln Val Ser Lys Pro Leu Gln Asp Asn Glu Leu Pro Gly Leu Asp Glu
353      290     295     300
355 Arg Pro Ala Pro Ala Leu His Ala Gln Asn Phe His Lys His Glu Phe
356 305      310     315     320
358 Trp Ser Ser Pro Phe Arg Ala Leu Lys Pro Arg Thr Ala Arg Lys Asp
359      325     330     335
361 Arg Lys Lys Lys Asp Gln Asp Thr Phe Thr Ala Ala Ser Ser Gln Val
362      340     345     350

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VERIFICATION SUMMARY

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L:28 M:220 C: Keyword misspelled or invalid format, [(A) APPLICATION NUMBER:]

L:29 M:220 C: Keyword misspelled or invalid format, [(B) FILING DATE:]